Dispersal Capability as an Indicator of Genetic Variation

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Highly mobile animals such as birds have great capabilities for dispersal. This scattering of genes tends to cause little geographic variation. Conversely, philopatric populations may display significant interdeme genetic variation. Dispersal capability, however, is not always negatively correlated with geographic variation. In a study of thick-billed murres (*Uria lomvia*), Birt-Friesen *et al.* (1992) found no significant genetic differences between north Atlantic colonies.

Thick-billed murres are a highly philopatric species of seabird. They come ashore only to breed and, after migrating extraordinary distances, return to their natal cliff colonies to procreate. They range throughout the arctic in areas deglaciated only 10,000 years ago. Though colonies are relatively young, they show many morphological differences, suggesting the possibility of significant genetic variation.

To quantify genetic variation between these colonies, Birt-Friesen *et al.* sequenced a 307bp region of the mitochondrial cytochrome *b* gene. They took samples from 5 Atlantic and 2 Pacific colonies. The mtDNA showed 17 genotypes among all *U. lomvia.* Of the 16 nucleotide substitutions, 12(75%) occurred in the third codon base. The remaining 4(25%) substitutions involved first positions; 2 of these cause amino acid changes. Genotypes 1-15 occur only in Atlantic colonies and varied significantly from genotypes 16-17 occurring only in the Pacific. No significant variation occurs within Atlantic populations where 27% of the genotypes comprise 95% of the population.

While the genetic variation between Atlantic and Pacific populations agrees with their geographic isolation, the lack of Atlantic interdeme genetic variation is unexpected. Birt-Friesen *et. al* expected significant interdeme genetic variation because of, 1) extreme natal philopatry, 2) significant interdeme morphological variation, and 3) genetic variation in other bird species with similar life histories. Some small amount of gene flow, counteracting genetic drift, could explain this inconsistency between indirect evidence and sequencing data. Additionally, large founder effects might produce interdeme genetic similarities.

This study suggests dispersal capability alone cannot predict geographic variation. Even when considering other indirect evidence such as morphology, variation measured by DNA sequencing may not match the expected significant amount of genetic differences. Mechanisms such as gene flow and founder effect may be influential enough to keep genetic variation low.

Literature Cited

Birt-Friesen, V. L., W. A. Montevecchi, A. J. Gaston, and W. S. Davidson. 1992. Genetic structure of thick-billed murre (*Uria lomvia*) populations examined using direct sequence analysis of amplified DNA. *Evolution* 46(1):267-72.